

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lambert, Lewis H., Jr.
- (ii) TITLE OF INVENTION: Improved Therapeutic Compositions Comprising Bactericidal/Permeability-Increasing (BPI) Protein Products
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/372,104
 - (B) FILING DATE: 13-JAN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sharp, Jeffrey S.
 - (B) REGISTRATION NUMBER: 31,879
 - (C) REFERENCE/DOCKET NUMBER: 27129/33071
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 31..1491
- (ix) FEATURE:

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(A) NAME/KEY: mat_peptide
(B) LOCATION: 124..1491

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rBPI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC	54
Met Arg Glu Asn Met Ala Arg Gly	
-31 -30 -25	
CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA	102
Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile	
-20 -15 -10	
GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC	150
Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile	
-5 1 5	
TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG	198
Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu	
10 15 20 25	
CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT	246
Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
30 35 40	
AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	
ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
60 65 70	
GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGC	390
Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	
AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC	534
Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
125 130 135	
CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGC TGG	582
His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp	
140 145 150	
CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG	630
Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
155 160 165	

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ATG Met 170	AAC Asn	AGC Ser	CAG Gln	GTC Val	TGC Cys 175	GAG Glu	AAA Lys	GTG Val	ACC Thr	AAT Asn 180	TCT Ser	GTA Val	TCC Ser	TCC Ser	AAG Lys 185	678
CTG Leu	CAA Gln	CCT Pro	TAT Tyr	TTC Phe 190	CAG Gln	ACT Thr	CTG Leu	CCA Pro	GTA Val 195	ATG Met	ACC Thr	AAA Lys	ATA Ile	GAT Asp 200	TCT Ser	726
GTG Val	GCT Ala	GGA Gly	ATC Ile 205	AAC Asn	TAT Tyr	GGT Gly	CTG Leu	GTG Val 210	GCA Ala	CCT Pro	CCA Pro	GCA Ala	ACC Thr 215	ACG Thr	GCT Ala	774
GAG Glu	ACC Thr	CTG Leu 220	GAT Asp	GTA Val	CAG Gln	ATG Met 225	AAG Lys	GGG Gly	GAG Glu	TTT Phe	TAC Tyr	AGT Ser 230	GAG Glu	AAC Asn	CAC His	822
CAC His 235	AAT Asn	CCA Pro	CCT Pro	CCC Pro	TTT Phe 240	GCT Ala	CCA Pro	CCA Pro	GTG Val	ATG Met	GAG Glu 245	TTT Phe	CCC Pro	GCT Ala	GCC Ala	870
CAT His 250	GAC Asp	CGC Arg	ATG Met	GTA Val	TAC Tyr 255	CTG Leu	GGC Gly	CTC Leu	TCA Ser	GAC Asp 260	TAC Tyr	TTC Phe	TTC Phe	AAC Asn	ACA Thr 265	918
GCC Ala	GGG Gly	CTT Leu	GTA Val	TAC Tyr 270	CAA Gln	GAG Glu	GCT Ala	GGG Gly	GTC Val 275	TTG Leu	AAG Lys	ATG Met	ACC Thr	CTT Leu 280	AGA Arg	966
GAT Asp	GAC Asp	ATG Met	ATT Ile 285	CCA Pro	AAG Lys	GAG Glu	TCC Ser	AAA Lys 290	TTT Phe	CGA Arg	CTG Leu	ACA Thr	ACC Thr 295	AAG Lys	TTC Phe	1014
TTT Phe	GGA Gly	ACC Thr 300	TTC Phe	CTA Leu	CCT Pro	GAG Glu	GTG Val 305	GCC Ala	AAG Lys	AAG Lys	TTT Phe	CCC Pro 310	AAC Asn	ATG Met	AAG Lys	1062
ATA Ile 315	CAG Gln	ATC Ile	CAT His	GTC Val	TCA Ser 320	GCC Ala	TCC Ser	ACC Thr	CCG Pro	CCA Pro	CAC His 325	CTG Leu	TCT Ser	GTG Val	CAG Gln	1110
CCC Pro 330	ACC Thr	GGC Gly	CTT Leu	ACC Thr	TTC Phe 335	TAC Tyr	CCT Pro	GCC Ala	GTG Val	GAT Asp 340	GTC Val	CAG Gln	GCC Ala	TTT Phe	GCC Ala 345	1158
GTC Val	CTC Leu	CCC Pro	AAC Asn	TCC Ser 350	TCC Ser	CTG Leu	GCT Ala	TCC Ser	CTC Leu 355	TTC Phe	CTG Leu	ATT Ile	GGC Gly 360	ATG Met	CAC His	1206
ACA Thr	ACT Thr	GGT Gly	TCC Ser 365	ATG Met	GAG Glu	GTC Val	AGC Ser	GCC Ala 370	GAG Glu	TCC Ser	AAC Asn	AGG Arg	CTT Leu 375	GTT Val	GGA Gly	1254
GAG Glu	CTC Leu	AAG Lys 380	CTG Leu	GAT Asp	AGG Arg	CTG Leu	CTC Leu 385	CTG Leu	GAA Glu	CTG Leu	AAG Lys	CAC His 390	TCA Ser	AAT Asn	ATT Ile	1302
GGC Gly 395	CCC Pro	TTC Phe	CCG Pro	GTT Val	GAA Glu 400	TTG Leu	CTG Leu	CAG Gln	GAT Asp	ATC Ile	ATG Met 405	AAC Asn	TAC Tyr	ATT Ile	GTA Val	1350
CCC Pro 410	ATT Ile	CTT Leu	GTG Val	CTG Leu	CCC Pro 415	AGG Arg	GTT Val	AAC Asn	GAG Glu	AAA Lys 420	CTA Leu	CAG Gln	AAA Lys	GGC Gly	TTC Phe 425	1398

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CCT CTC CCG ACG CCG GCC AGA GTC CAG CTC TAC AAC GTA GTG CTT CAG	1446
Pro Leu Pro Thr 430 Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln 440	
CCT CAC CAG AAC TTC CTG CTG TTC GGT GCA GAC GTT GTC TAT AAA	1491
Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys 445 450 455	
TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC	1551
ACCGGCTGCC TTTCCCCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTGCAAAC	1611
TCTTCGACTC AGATTCAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAGAGTG	1671
CATGGTGTGT ATTTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT	1731
CCTCCAGGAA TCGTGTTTCA ATTGTAACCA AGAAATTTCC ATTTGTGCTT CATGAAAAAA	1791
AACTTCTGGT TTTTTCATG TG	1813

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val	
-31 -30 -25 -20	
Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val	
-15 -10 -5 1	
Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala	
5 10 15	
Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys	
20 25 30	
Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly	
35 40 45	
His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser	
50 55 60 65	
Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser	
70 75 80	
Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe	
85 90 95	
Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile	
100 105 110	
Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr	
115 120 125	
Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His	

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130		135		140		145
Ile Ser Lys Ser	Lys Val Gly Trp Leu	Ile Gln Leu Phe His Lys Lys				
	150	155			160	
Ile Glu Ser Ala	Leu Arg Asn Lys Met	Asn Ser Gln Val Cys Glu Lys				
	165	170			175	
Val Thr Asn Ser	Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu					
	180	185			190	
Pro Val Met Thr	Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu					
	195	200			205	
Val Ala Pro Pro	Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys					
	210	215			220	225
Gly Glu Phe Tyr	Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro					
	230	235			240	
Pro Val Met Glu	Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly					
	245	250			255	
Leu Ser Asp Tyr	Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala					
	260	265			270	
Gly Val Leu Lys	Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser					
	275	280			285	
Lys Phe Arg Leu	Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val					
	290	295			300	305
Ala Lys Lys Phe	Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser					
	310	315			320	
Thr Pro Pro His	Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro					
	325	330			335	
Ala Val Asp Val	Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala					
	340	345			350	
Ser Leu Phe Leu	Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser					
	355	360			365	
Ala Glu Ser Asn	Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu					
	370	375			380	385
Leu Glu Leu Lys	His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu					
	390	395			400	
Gln Asp Ile Met	Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val					
	405	410			415	
Asn Glu Lys Leu	Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val					
	420	425			430	
Gln Leu Tyr Asn	Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe					
	435	440			445	
Gly Ala Asp Val	Val Tyr Lys					
	450	455				

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